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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/987,967

DATE: 11/21/2001
TIME: 10:25:14

Input Set : A:\PF268D1C1SEQLIST.txt
Output Set: N:\CRF3\11212001\I987967.raw

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3 <110> APPLICANT: Wei et al.
5 <120> TITLE OF INVENTION: Human Hematopoietic - Specific Protein
7 <130> FILE REFERENCE: PF268D1C1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/987,967
C--> 9 <141> CURRENT FILING DATE: 2001-11-16
9 <150> PRIOR APPLICATION NUMBER: PCT/US96/04930
10 <151> PRIOR FILING DATE: 1996-04-11
12 <150> PRIOR APPLICATION NUMBER: 08/837,029
13 <151> PRIOR FILING DATE: 1997-04-11
15 <150> PRIOR APPLICATION NUMBER: 09/265,977
16 <151> PRIOR FILING DATE: 1999-03-11
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 833
24 <212> TYPE: DNA
25 <213> ORGANISM: human
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (42)..(608)
30 <223> OTHER INFORMATION:
32 <220> FEATURE:
33 <221> NAME/KEY: sig_peptide
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38 <221> NAME/KEY: mat_peptide
39 <222> LOCATION: (108)..()
40 <223> OTHER INFORMATION:
43 <400> SEQUENCE: 1
44 ctcaaccaca gactacactt gctgaactgg ctctctggggc c atg agg ctg tca ctg 56
45 Met Arg Leu Ser Leu
46 -20
48 cca ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc 104
49 Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu
50 -15 -10 -5
52 ggg gac agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag 152
53 Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu
54 -1 1 5 10 15
56 gag atg tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc 200
57 Glu Met Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys
58 20 25 30
60 aga gct gtg gct tac cag atg tgg caa aat ctg gca aag gca gag acc 248
61 Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu Ala Lys Ala Glu Thr
62 35 40 45
64 aaa ctt cat acc tca aac tot ggg ggg cgg cgg gaa ctg agc gag ttg 296
65 Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg Glu Leu Ser Glu Leu

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66          50          55          60
68 gtc tac acg gat gtc ctg gac cgg aac tgc tcc cgg aac tgg cag gac 344
69 Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser Arg Asn Trp Gln Asp
70          65          70          75
72 tac gga gtt cga gaa gtg gac caa gtg aaa cgt ctc aca ggc cca gga 392
73 Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg Leu Thr Gly Pro Gly
74 80          85          90          95
76 ctt agc gag ggg cca gag cca agc atc agc gtg atg gtc aca ggg ggc 440
77 Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val Met Val Thr Gly Gly
78          100          105          110
80 ccc tgg cct acc agg ctc tcc agg aca tgt ttg cac tac ttg ggg gag 488
81 Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu His Tyr Leu Gly Glu
82          115          120          125
84 ttt gga gaa gac cag atc tat gaa gcc cac caa caa ggc cga ggg gct 536
85 Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln Gln Gly Arg Gly Ala
86          130          135          140
88 ctg gag gca ttg cta tgt ggg gga ccc cag ggg gcc tgc tca gag aag 584
89 Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly Ala Cys Ser Glu Lys
90          145          150          155
92 gtg tca gcc aca aga gaa gag ctc tagtcctgga ctctaccctc ctctgaaaga 638
93 Val Ser Ala Thr Arg Glu Glu Leu
94 160          165
96 agctggggct tgctctgacg gtctccactc ccgtctgcag gcagccagga gggcaggaag 698
98 cccttgctct gtgctgccat cctgcctccc tcctccagcc tcagggcact cgggcctggg 758
100 tgggagtcaa cgcttcccc tctggactca aataaaaccc agtgacctca aaaaaaaaaa 818
102 aaaaaaaaaa aaaaa 833
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 189
107 <212> TYPE: PRT
108 <213> ORGANISM: human
110 <400> SEQUENCE: 2
112 Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
113          -20          -15          -10
116 Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
117          -5          -1 1          5          10
120 Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
121          15          20          25
124 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
125          30          35          40
128 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
129          45          50          55
132 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser
133          60          65          70
136 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
137 75          80          85          90
140 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
141          95          100          105
144 Met Val Thr Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
145          110          115          120
```

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```

148 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
149          125          130          135
152 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
153          140          145          150
156 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
157 155          160          165
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161 <211> LENGTH: 28
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <221> NAME/KEY: Primer_Bind
167 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI restriction site
168      encoding a start AUG, followed by 19 nucleotides of the hHSP
169      coding sequence beginning with the first base of the 23rd codon.
171 <400> SEQUENCE: 3
172 cgcggatccg acagggcgcc actcacag                                28
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <221> NAME/KEY: Primer_Bind
182 <223> OTHER INFORMATION: Synthetic primer containing an Xba I restriction site
183      followed by 21 nucleotides complementary to the last 21 nucleotides
184      of hHSP including the stop codon.
186 <400> SEQUENCE: 4
187 gcgtctagag aggtcactgg gttttatttg                                30
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 34
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <221> NAME/KEY: Primer_Bind
197 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI restriction site
198      followed by 19 bases of the sequence of hHSP.
200 <400> SEQUENCE: 5
201 cgcggatccg ccatcatgag gctgtcactg ccac                                34
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 30
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <221> NAME/KEY: Primer_Bind
211 <223> OTHER INFORMATION: Synthetic primer containing an Xba I restriction site
212      followed by nucleotides complementary to the last 21 nucleotides of
213      hHSP including the stop codon.
215 <400> SEQUENCE: 6
216 gcgtctagag aggtcactgg gttttatttg                                30

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219 <210> SEQ ID NO: 7
220 <211> LENGTH: 34
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <221> NAME/KEY: Primer_Bind
226 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI site, an AUG start
codon
227 and 16 nucleotides thereafter.
230 <400> SEQUENCE: 7
231 cgcccatccg ccatcatgag gctgtcaactg ccac 34
234 <210> SEQ ID NO: 8
235 <211> LENGTH: 57
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <221> NAME/KEY: Primer_Bind
241 <223> OTHER INFORMATION: Synthetic primer containing an Xba I site, a stop codon,
242 9 codons forming hemagglutinin tag and 18 bp of 3' coding sequence.
244 <400> SEQUENCE: 8
245 cgctctagat caagcgtagt ctgggacgtc gtatgggtag agctcttctt ctgtggc 57

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date